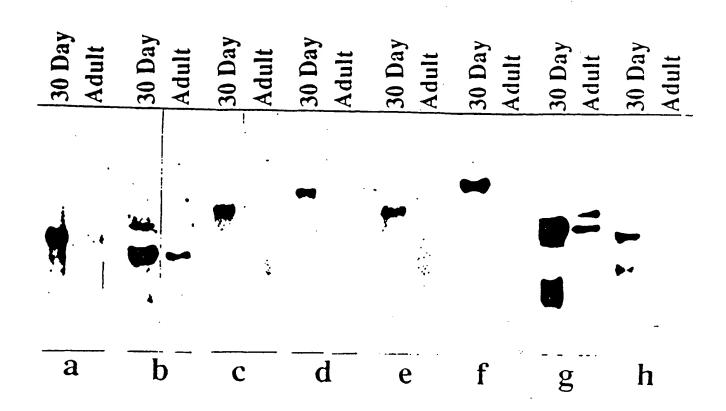




FIGURE 2



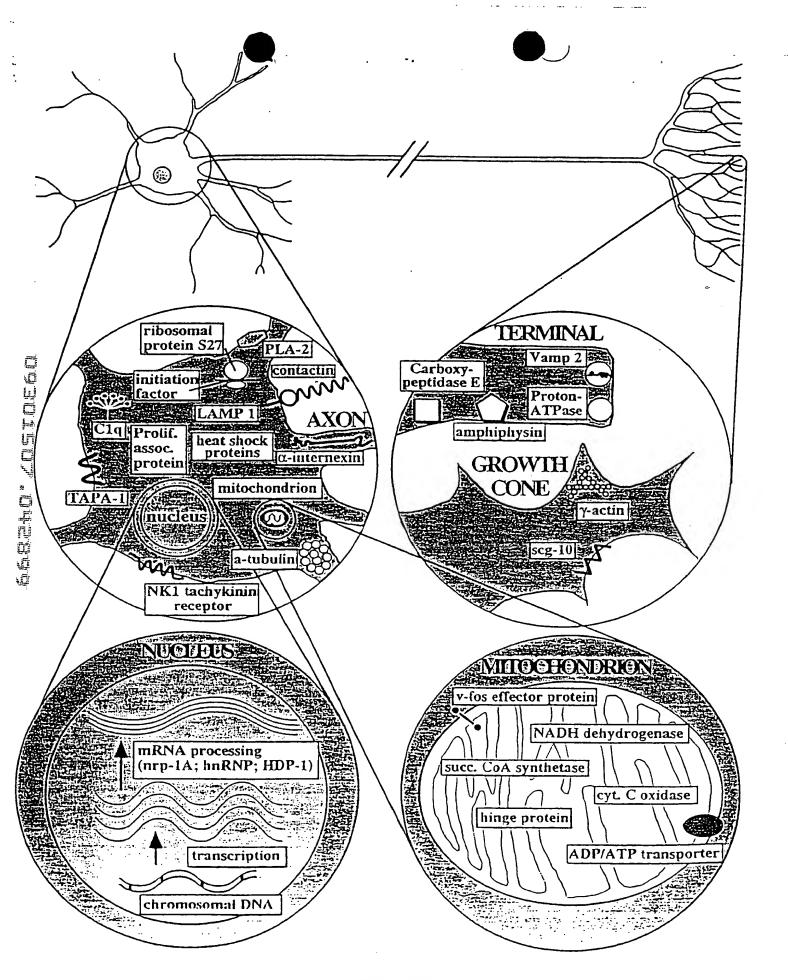


FIGURE 4

pKVC43:

CCTGGCTGCCTCAACCCCACTCCCAGGGAGACCAAAAGCCTTCATACATCTGAA AT

SEQ ID. NO.: 2

pKVC2B:

GCGACGGACGAGATGTCTTCGGTGTCCTTGCGTTCGCTACCAGGTCAAAATGCAAATCTTCGTGAAAACCCTGACGGGCAAGACCATCACCC

SEQ ID. NO.: 3

pKVC15:

SEQ. ID. NO.: 4

>pKVC24BR

poly(T)ATCCATACTTGCTATTTATTTAGGCTTCTAGTTTGGAACAAAAGGNCAAGAGTTAAAAAAAT GCCAACATTTCAAGGACCCTTGTT

SEQ ID. NO.: 5

pKVC26B:

CTTCCCCCACTCATCCCTGGTCCCTTGTgCCCCTTGGCCCTTTACCCCAAGCACCACCCCACAG ACTGGGGACCAGCCCCCTCTCCTGCCTATGTCTCgCCCCAAAT

SEQ ID. NO.: 6

pKVC50B:

CCTTCCCTTACTTTAATAGTTCGGTAGTACGGANGTTAAATCTTCAGGTCGGTGGTACGCAGCCGGCAACCATGCAATGGATTNAAGGTNGGTAATGGTACAATTGGCCTATGCCCACTTT

SEQ ID. NO.: 7

pKVC85B:

CTTTAGAGCGCACTCAGGGGCACTTGNAAGGGCTTCTCACGAGCGTGGCTGTGGCCATCTGTGGAAAGAGCTTCTCGCAGTGNTCGGTNGNNTTATCCCCCACGCCCNTAGNGCACTACTC

SEQ ID. NO.: 8

pKVC100:

TTAGTTTCACATTCAAGGGGCTTATGAAGAGATGCAAGTCAGGATACATAGGCTTGATTCTTGGCAGCTTAaTGAGTaTTCACtGAGGCACTtG

SEQ ÎD. NO.: 9

pKVC94B:

pKVC90B:

TTTATTATGCACACGTTGTTCAAATAAACCAGTGTGGGATGTTAAGACTATCAATTAATGGTGGGATTA TGTTTGGCATTTTATTNNTTATAAATATATTTTTTTCTGAATGTGTCCTGAGNTCCAAAGAGGTTGGG GGNGGGGGNG

SEQ ID. NO.: 11

pKVC91B:

TTTCCTTGGGTTGCTGGATTAATCTTTAATAACAATATATAGAATTGTAGACTGATGTTTTAGTG TTTTTCCAACACACACACAAACATAAAAATAAAAACAAGTCGGACCGCTACTTCTGTGTAAATCAAGATCNTT GGGGAA

SEO ID. NO.: 12

pKVC101B:

CCTGGCCAGCGGCCACGAAGGCAAGATCGGTCGTTGTGCTTGTGTTTTCCAAGGAGACGANCC NATNANCTGTAAATATGTACACGTNTCTGTCTGTGTGTCCTTCGNGGNAGG

ATGGTCGGNTCTATTTAAA

SEQ ID. NO.: 13

pKVC103fB:

ATGGGCTTANAANAATTAT

SEQ ID. NO.: 14

pKVC105:

TTTACTGACAAGCATGGGGAAGTGTGCCCAGCTGGCTGGAAGCTGGCAGTGATACCATCAAGCCTGATG
TCcAGAAGAGCAAAGAATATTTCTCTAAGCAGAAGTGAGCCCTAGGCCTTTT

SEO ID. NO.: 15

pKVC107:

CGGCTTCcTGGGCTTTATCGTATGAGCCCATCACATGTTTACTGTAGGAATGGATGTAGACACACGAGC ATACTTTACATCAGCCACTATAATTATTGCCATTCcTACCGGGGTGAAAGT ATTTAGTTGACT

SEQ ID. NO.: 16

pKVC1B:

GGAGCTTGAAGAAGAAGTTTTTTACCACCGTCTTTTTCTACTTTATACAGAAGTAGATATTCCTGCGAA GAAGAATAATTTGGGGTAATATGCAAGCTAGTAGATGTGGCACAGCAAATC ATATAATAAA

SEQ ID. NO.: 17

pKVC5B:

pKVC7:

CACCTTCCTGAAACACCTGTGGCTTTGACTTTGTTATTGATCCAGATTATTCTCCTTGCATTGGGGAAA ATATCTTTCATATTTCACTGTAAGGGATGGTTTTGCGAGAGTAAGTTAATGTCAAGACAAACTGCCAAT ACAAGAGCCCAATGATATTAATTACATGAGAAAAAGTAACTA ATACATCC

SEQ. ID. NO.: 19

>pKVC55R

SEQ ID. NO.: 20

pKVC13B:

GCTACGGTCGACATCACCATCTTTATCCCTTCCAGCCCTTTGCTGGGTCGCGGGCCTTGGGAAGATGCC AAAGAGCCGAGCAGTGGTGGCCAGCGGGCAGAGTGTCCCTGCTTGGGCCAGGAAAGCTTTACCTTC TCTGAGCGCCTCTGCCTGAGAGATCGATGGTCTGTGGCTCTA GGAGACCACGTCTTGGAGTG

SEQ. ID. NO.: 21

>pKVC6R

SEQ ID. NO.: 22

pKVC16B:

SEQ. ID. NO.: 23

>pKVC74F

SEQ ID. NO.: 24

pKVC29B:

>pKVC79R

poly(T)GTGTTAAGTGGTCTTTATTGGGGTGTCACATTAGGTTATCTTCATTATCAGTTCTTCAG TTAATTGTACAAGTATGATAAGTTATTTTATATCTGACGTGGGAATTTAAATGTAAAATAAAATACAAAA TACATCTGTGGTTTAATGAACACTCAATGAAGAC

SEQ ID. NO.: 26

pKVC30:

ACAACAACTGTTGCAGGTGCTTTTGTGTGGAGTGTGTGGATCTGTTGGTGGGGCCGGGGGGCCCAGGAC TCAAGGAGGACCCCTGGAACTGCTACATGTGCGGGCACAAGGGCACCTACGGGCTGCTGCGGCGGCGG ACGACTGGCCCTCGCGGCTGCAGATGTTCTTTGCCAATAACCACGACCAGGAGTTTGACCCTCCGAAGT TTACCCA

SEQ. ID. NO.: 27

>pKVC7R

poly(T)ACACAGAACAAGAAATTTTATTATCTCGAATGCTGGTGCATAAGCAATAACAAGCTCATCAA TTAGAGGAGGAGACAGAGGGAAACTTCAGATACTGATGAGGATTTCTGGGCAGGTTTAAAACCTTTAAA GATTGAGGCCATAATTGTtCAGTCTTTTTTT

SEQ ID. NO.: 28

pKVC32B:

CCTTGCCAAGGCCGAGGCTCCACAGGAATCAGAGTTGGGACGACNNNNGAAGGAAGCGTTTGGCTTCAC ATTCTAGAGAAAGAAGACCCTACTGGGCTGCAGACCCCTCCAGGGCTGTAGGAAAGCTGCTGGACCTCT TCTGCTTCTCCCCAACCACTCTGCCACTCTGCCAGTTACCAG

SEQ. ID NO.: 29

>pKVC45BR

TTCAGAATACTGTTTTTTTTTTTTTTAATTTGTTTTGGTTTTGTTTTTAATTTAAAGAAAGGT ATTTTGCTTGCAGGAAAAATACTCCAGATTCATTTTAATGAGAATCTTTGAAATGTATTTATCTTTAGG GCATTTGGGGCAACTTTAATGCCTGTTGGCCTCCGGCCTTCCTGGAAATAAAAGGTCCAACGG

SEQ ID. NO.: 30

pKVC34B:

CCTGCCCCACGCCATCCTGGACCTGGACCTGGCCGGGACCTGACGGACTACCTCATGAAGATCCT CACAGAGCGCGGCTACAGCTTCACCACCACCGCCGAGCGGAAATTGTGCGTGACATCAAGGAGAAGCTC TGCTACGTGGCCTTGGACTTCGAGCAGGAGATGGCCACCGCCGCGTCCTCGTCCTCCTGGAGAAGAGCT ACGAGCTGCCCGAC

SEQ. ID. NO.: 31

>pKVC89BF

ATTGTGATAGAAGACCACGGTGGGTTCAANCANGTTGAAGNAGTTCCGCNTTTCCCCTCCGGGGGAAAG GTTGTCGATGTCTNTTGGTNNTAAGTANTCACCCATNCATTGTTGACAAGGNTCANTCCCGAAGGGTCA TTCTTGAGTAGTAGACCAATATTNTAAAAATAATTTNAATCCTT

pKVC34:

SEQ ID. NO.: 33

pKVC36B:

ACGCTCGTTTTCCAAAGAGAAGAGCGTTGTTTAGAGTAGCGAAATTCGAAGGCTGCTTAGGCGCATTGT AAAGCTGTTGGGGAAATAACTCCACAAGTTTCGTGAGTGGAAATGTAGTGCTCGAAACACATTCTGCTT TAAAAGGTTGTAACAAATACAAACAAATTTAAAAAAAAGCTCT CGAAAA

SEQ ID. NO.: 34

pKVC43rB:

CTGGAGCGCAAGTACTCCGTGTGGATCGGTGGCTCCATCCCGGGCTTGGTGTCCCACCTTCCACAAGTG TTGATCACACAAGCCGGAGTACGCGCGCGGTTCGGCCCCCTTCATAGGCCACCGCAAAAACTTTTAGGC GGGCTCTTACNTTAGAGGCGGTACACACCTTCTTG

SEQ ID. NO.: 35

pKVC73:

SEQ ID. NO.: 36

pKVC79B:

GTCTTGATACAAAGCTTCTGTGCTAATCCAGACTATTTAGGCAGGGGCAATAGGGTGTAAAATGTATCT GCTCTCTTCAAACGCGGCTAANGNTCTAGTCCATGTCCCNCCNNGCAACCNNCAANATCCCACNAGGGG GNAGNTCG

SEQ ID. NO.: 37

pKVC81B:

SEQ ID. NO.: 38

pKVC83B:

CATCTAGATANTCTTGGNGATTGGGGCCTCTAGNTGATTGCTCGAGCGGCCGCCAGTGTTTTTAAAGA CTGGCTCAGGGCCTGTGCGAGGTGCTGGTGGTGACCAAGGAGGTGGAGGAAAAGGGCTGCTGGNCT GCGGNACAGTACTGACCCCGCGGAGGTAGTAGCAACCAGGTCCACCGTACCCCTGCGAGTCCCCCGCTG CCAATCCCC

pKVC87B:

CCACCAAGAAGCTGGACCTGTGGATGCTGCCTGAGACACTCATTATCCACCTGAAGCGCTTCTCTTACA CCAAGTTCTCCCGCGAGAAGCTGGATACCCTTGTGGAGTTTCCCATCCGGGACCTGGAACTTCTCCGAG TTTGGCATCAAGTCCGTAGGAACGAGTCGGCTCCGGAGCTGTACAAATACGCATCTCATCGNGGGNTNC CATCNCATTNATGGGGG

SEQ ID. NO.: 40

pKVC104fB:

GGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGGCGCCAGTGTGCTCTAAAGCCAAAATATATTTGA GCCAAATGTTCCGAGGATGAGTCAGGCTGTCTTCGGGGGCAGNAAAGGCTTCACACGGGACAAGTGGAT GGNTTGGAGGAATGNATGNTCCGCAACCATGGGCT

SEQ ID. NO.: 41

pKVC104:

SEQ ID. NO.: 42

pKVC109B:

GCCAGATTTACATAAGAACATGCTTAACAGACGATCTTTTAGCTGACGTCTTACCAGNAATCGCCCAAG TCCGCACGGTAAGTAAAGAGGAGGCCCGCCAGGTCAGAGTTTGCTTAGCAATAGGGTCAGGTCACTAAA ACTGTAAATCCATTGCGAGAGGGGGACGCCTCCGCTCAAGCT TGGCTGGGCTTCGGC

SEQ ID. NO.: 43

pKVC89B:

TCA

SEQ ID: NO .: 44

pKVC115:

*GCGCAGGCACAGCTGGTGAGGGGCGAGGCCGCAGACGCCAAGGTGGCCACCATGGTCCGGAGTGCCTGC
AGGTAGTGGGCTTCGTCACCGAGCTTCGTGGGTTGGATCGGCATCATCGTCACCACCGACCAACGACT
GGGTGGTGACCTGCGGCTACACCATCCCCACCTGCCGCAAGCTGGACGAACTGGGCTCCAAGGGGCTGT
GGGCAGACTC

SEQ ID. NO.: 45

FIGURE 5F

pKVC20fB:

CAAACCCATGCATACCACATAGTCAACCCTAGCCCATGGCCACTTACAGGAGCCCTTtCAGCCCTCTTA
ATAACCTCAGGCCTGGCTATATGATTCCACTACAACTCAACACTGCTGTTAACCCTTGGAATAACTACC
AACCTACTAACTATATATCAATGATGACGAGACATTATCCGAGAAAGCACATTCCAAGGCCATCATACA
CCTATCGTTCAAAAAGG

SEQ ID. NO.: 46

pKVC7B:

SEQ ID. NO.: 47

pKVC92:

AGACCAGCCGGTGACAACCACTAATCAAGTTCCATAACTATATAGCGCCGCAATTCCCATGGCCTCCTC ACTAAAGAACCCTGAGTCACCTGTATCATAAATCACCCAATCACCTGCACCGTTAAACTAAATACGAC TTCTACCTCATCTTCCTTTAAAATATAACAAGCAGTTAATAATTCTGCTAACACCCCCGTAATAAACAT TGCTAGTA

SEQ ID. NO.: 48

pKVC8: TGAGGTTGATTATTGTGGTGGTATTGTTCACTGTGTAGAAATAGTAGGAGTA

SEQ ID. NO.: 49

pKVC8B:

SEQ ID. NO.: 50

pKVC14:

pKVC16:

TGGTGACACGTCTTTCAGTCACCAGTGGAGATCACCAGGAGCATCAGCAGGAAGAGCCAGTGGGCCC ACAAGCTTAGCAAGTTGATCAGGATAGGGTTATTTGGTGGATAGACCATGAGTGTCAGGGACCTCCCAC TGGACACCACCCCAGAGGCTCAGGATGCTTTTCGAGGGAGAAAGGAGAAAGACCTCTACTGAGGGAAC AGCTGGCCGTGTGTGGTGGGCTGAGGTGACGTACAGGGGCAGAGCTTTCGAGGGATTTTTCAGATGATCC

pKVC20rB:

SEQ. ID. NO.: 53

>pKVC59BR

SEQ ID. NO.: 54

pKVC21B:

SEQ. ID. NO.: 55

>pKVC61BF

poly(T)CCCNAGNGCACACNGGNGGCCNTAANNAGNGGNTCCNAGCNCGGNACCNAGNTTGAGGCATA GCTTNAGNATTCNATAGTGNANCACAAATAGCNTGGGGNAATCANGGNCAAAGCCNTTTCCCGTGNGAA ATTGTNATCCNNTCANAATTCCNCACAANATACGGGCCNGAAGCATAAAGNGTAAAGCCCGGGGGGCCC AANGNGGGNGCNAACTCACATTTAATNGCG

SEQ ID. NO.: 56

pKVC23:

SEQ. ID. NO.: 57

>pKVC9R

pKVC28B:

SEQ ID. NO.: 59

pKVC29:

SEQ ID. NO.: 60

pKVC38:

CGAATCTGTTGTAGCAGTTTCAAATGATTGTGTGGATATTGGATGTTTAACCTTTACCATTTGCTTTGT ATCGACACACTTTTCATTTTAAGTGTTAACTCATGTTACTGTTACTTTAGGAATAATGCAAATCCAACC TTCATCCAGTGATGAGAATAGCAGTATGATAGGAATTTGCTCAATGTGCTTTAAATGAGTAATTGCTTT ATCTTTTTAGTATCTGATAGACTTTGCATGACACGGTACACTCCTAATTATGCATTCTTTAGTTTCCA AATCTTAACCTAAGACATTCTATATTAACTGATGGGTAGCTGAG

SEQ ID. NO.: 61

pKVC48B:

GGTTTTGCAGGGGCAAGTGGGCCCCGCCGCTGGGTGAGAACCCCGCCGCACACTGCAGTGGGTGCC TGGACCCCGCAGCAGCGCTGAGCAGACGGTGGACTCTGGGCTGTGGCCTTTCTTGGGCCCACTGGGGCC GGCTCTTGTATATAGCTGGGGCTCATGGGCATGACCCCTTTTTTAAAACCTTGGGTCTTAGGACACCTG GGTTTACCCTCAACTAAGGGAGGGTGGGAAAGGGATTTACTTGGGGTCTCAATAATTTACGATATCCCT TTAAGGTTGACCATTAAAACTGTCCCA

SEQ ID. NO.: 62

pKVC51B:

CCTCTTAATAACCTCAGGCCTGGCTATATGATTCCACTACAACTCAACACTGCTGTTAACCCTTGGAAT AACTACCAACCTACTAACTATATATCAATGATGACGAGACATTATCCGAGAAAAGGCCATCATACCACCTATCGTTCAAAAAAGGCCTTCGATACGGAATAATCCTCTTTATCATCTCAGAGGTATTCTTTTCGCAGGCCTTTCTTCTGGGGCCTTTGTTACCACTCAAGCCTAGCCCCAACCCCCCGTAGCTTAGGGGG

SEQ ID. NO.: 63

pKVC53B:

pKVC69:

TGGCTGTCATCTGGAGGCTTCTGCCTCAGCTCCTGAAGGCTGCTCCATTCCTTCTCGCGTGCTCCCGT CCATCTTCAAATTCTCAATGGCCCATCTTCTCACGCCTCCCATCCCTCTGCCTTCTTCTCTGTTTTAA GGTTCATGTGATTAGATCAAGCCCACTGATCAAGTCTCCCTATTTTAAGGTCAGTTCTGCCATAGAACA TAACATAATCACAGGAGTGACTGCACAGGCACGGGTTCCTGGGATTTTGGGCATGGAGTTGGGGG

SEQ ID. NO.: 70

pKVC74:

SEQ ID. NO.: 71

pKVC86:

SEQ ID. NO.: 72

pKVC96B:

ACTGGACCAAAATTGGTGTTTTGTTTTAACCTTGACTCTTCTTTTGATTATTTCTAATGCTACAAGAATG CTGTAAAGTGTCTTCTACAATGATGTAGCCCTGACAAGACATGTTTGGCAGTGTATAAAAATTAGGTAG GATTGTGCACTGATTCGACCATTGTGAAATCTTTTCTCAGTGGTAAGTGCATTCTCTAATAAAATTTAT GNAGGTGAAACAATCTTTGGNGCAATGGACCACTCATGCATCCATCCC

SEQ ID. NO.: 73

pKVC97B:

SEQ. ID. NO.: 74

pKVC103rB:

SEQ ID. NO.: 75

pKVC103:

CGGCCACTGGTCATCAGATGAGCATTTTGTGTGTTTTGAAGCTAGTAGCTATAGAAAAGATAGTTGTGCC CTGATAAAGTAGCTTTTTAAAAAAAAGTTTGGGTTAGTTTCACATTCAAGGGGCTTATGAAGAGATGCAA GTCAGGATACATAGGCTTGATTCTTGGCAGCTTAATGAGTCTTCACGAGGCACTGAAGGTGGAAGGGTG GAGTCCAGTAAĆTGCTCTGGAGCAGTGACTTCCCAATTCTGACGATCTCAACATTGTTTCTGAAGGACG TTGCCATCTTGGACACAGGAACGTGCTGTGGGGTGCCTGGCAGTGTCTGAGTAGTAGACTT

SEQ ID. NO.: 76

pKVC104rB:

SEQ ID. NO.: 77

pKVC107fB:

ATTACAACATCTAGAAGGCTTTCATCATACGATACAAAGCTCAGTTACAAATGTGCATCCTAGTATTTG GAAAACTAATACCTCTCTTAATGTAACATGAAAAAATTATTTCTTATGTCCTTTTTCAGGACTCCTCTT TTATTTTTTGGTATTTTATCTTTTATGGCCACCTTGGCCTTCTGGCCAATGTGTTATGCAGTGAAAATG CTTGTGGGCAGAGGATGCCCTACAGCGCAAAAATACCGCGCACATGGGTTTCCCAGGTA

SEQ ID. NO.: 78

pKVC107rB:

TTTTGTTTTATCCGTTTATTAGTACATGGGCGTCGGGAGGATGATTTACTCATCATCTTGTATTACCAG AGGTAGAGCATAATGCCATCTGCTAGGGATCCAGTTCGACAGCACCTCAAAACACTAGTCTGCTCACTC ACCCTATAGGGCTTGNTCATTCCACTTGGGATGGAAGAACACAGTGCCTTTAATGCAAATGGGCCCCAG GCAAGGAATTAACCATTGGCTTCATGGCTCATGAAGGAATACAGNCNNATTTAANGCGNGGCAGGCAGG AAGCCTTTGNGCTA

SEQ ID. NO.: 79

pKVC124:

SEQ ID. NO.: 80

pKVC24B:

pKVC25:

SEQ ID. NO.: 82

pKVC40B:

SEQ ID. NO.: 83

pKVC43fB:

SEQ ID. NO.: 84

pKVC55B:

SEQ ID. NO.: 85

pKVC57B:

pKVC60fB:

SEQ ID. NO.: 87

pKVC60rB:

SEQ ID. NO.: 88

pKVC63B:

CCTACCCGGTTTTGGGATAATCTCACATATTGTTACCTACTATTCAGGTAAAAAAGAACCCTTTGGCTA CATGGGAATAGTTTGAGCCATGATATCAATCGGCTTCCTGGGCTTTATCGTATGAGCCCATCACATGTT TACTGTAGGAATGGATGTAGACACACGAGCATACTTTACATCAGCCACTATAATTATTGCCATTCCTAC CGGGGTGAAAGTATTTAGTTGACTGGCTACTCTTCATGGAGGGTAATATTAAATGGTCCCCTGCTATATT ATGAGCCTTAGGCTTTTATTTTCCCATTTACCGTAGGAGGGCCTAACGGGGATTGTACTAGCAAACTCT TCACTAGACAATGTTCTTCACGGCACATATTACGTGGGGGGCCACTGTCACTATGGCTTGTCAATAGGG GCAGTATTCGTATCATAGGGGGGTTCGTCC

SEQ ID. NO.: 89

pKVC64B:

pKVC66B:

SEQ ID. NO.: 91

pKVC82B:

GCCACCTGACCCTCCTAACCCATGGCTGTCTGATGATACTACTTTCTGGGAACTTGNAAGCAAGCAAAG AACCAAGTCAGCAGAGGGTAAAACGATGGGGTTTTGGCATGGATGAAGCATTGAAAGACCCAGTTGGGA GAGAACAGTTTCTTAAATTTCTAGAGTCAGAATTCAGCTCAGAAAATTTAAGATTCTGGCTAGNCAGTG GAAGNACCTGAAAGNAAAAGGTCTAATNAGGAGAAAGTTCCCTTTCCCGGAGATTCAGGGAAAATATGG GCAAAGNAATTTTCTTGGGCTCCCTGGGAGGCTTCCCCAGNTGCCCAATCCAAACCTTGGGGTTTTCCT NAAGGAGGGCTNATGGATT

SEQ ID. NO.: 92

pKVC110

SEQ ID. NO.: 93

pKVC134: Homologous to human alpha tubulin; Accession HSHA44G CCGCCAGTGTGCTCTAAAGTGTGGTACCCTGGTGGAGACCTGGCCAAAGTACAG CGAGCTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGC CTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTGTTCACTGGTATGTGGGTGAGGCATG GAGGAAGGAGGAGGAGGTTTTCTGAGGCCCGTGAGACATGGCTGCCCGTGAGACATGGCTGCCCTTGAGAAGGA TTATAGGAGGTTGGTGTGA

SEQ ID. NO.: 94

pKVC108: Homologous to Mouse Initiation factor eIF-4A;

Accession MMEIF4AL

pKVC105B: Homologous to Human mRNA for prolif. associated protein;

Accession HSPAG

GTCAGACACACTTTCTGAATCCTCTNAGGANGGTGATCCAGTTCATGAANATTCTCTGTAAAATNANT NTGGNAAACTANATNAGTGNNGATNCAGGTCTNGAGNNTCTCCTTCCAGTGNCTAAAAAGTNCACAGAN GNCAGGAACTNCCTATCTGCATGCAGTCACCAGTTCTCATNC TCTANGCA

SEQ ID. NO.: 96

pKVC92B: Human Mitochondrial hinge protein; Accession HSHINGE CCCAGCCTTCATGAGCTGGTCATCAGGATACTTTCTTATGGGNTNGANCATGCCANTTGCTTNTNCGNG TANATGTAAGTTCATGNCAACCNCATTTTTTTTCTAGCCTNNGGNCTNAAGGTNANTCGTCTCNTTANG CAGCNGANNCAGTTGNAGTCTNTCAAANGNNCACAAANACCTAA

SEQ ID. NO.: 97

SEQ ID. NO.: 98

pKVC90: Homologous to Human hnRNP core protein A1; Accession HSRNPA1 ACAACTTTGGCCGTGGAGGAAACTTCAGTGGCCGAGGTGGCTTTGGCGGCAGTCGAGGTGGTGGAT ATGGTGGCAGTGGGAGGTGGTATAACGGATTTGGTAACGATGGAAGCAACTTTTGGAGGTGGAAGCT ATAATGATTTTGGCAATTACAACAATCAATCTTCAAATTTTGGACCCATGAAAGGAGGAAATTTTGGAGGCCAGAAGCTCTGGCCCCTATGGTGGTGGAGGCCAATACTTT

SEQ ID. NO.: 99

pKVC86B: Homologous to Rat Ribosomal protein S27; Accession RRS27 GCGAAGGACCTCCTGCACACGTCCCCGGAAGAGGAGAAGAAGAAGCACAAGAAGAAGAAGCGCCTGGTGCAG AGCCCCAACTCCTACTTCATGGACGTGAAGTGCCCGGGGTGCTACAAAATCACCACCGTGTTTCCCT

SEQ ID. NO.: 100

pKVC82: Human Carboxypeptidase E; Accession HSCARBE
ATCTGCCATTTTAGACTTAAAGGAAATATTCCACGTGTTATTTACGATCCAGAAGTTTTTGAGTAATTC
TGGCTTTTAAAAACTAATGAAGTCCTTTTAGTGTAATGGTAACAGTGCCACATAGTGAATGCCACTGAA
AAGGTCAACAGCTACATTTTGGTGTTGTGAGCATTATACCGCAAGACTTACATAGTTCAGTATAA

pKVC80: Homologous to Rat VAMP-2; Accession RNVAMPB

SEQ ID. NO.: 102

pKVC79: Homologous to Bovine Nuclear encoded ADP/ATP transporter;

Accession BTADTPMT

GGATGATTGCCCAGAGCGTGACAGCGGTCGCAGGGCTGGTGTCCTACCCCTTTGACACTGTCCGCCGTA GATGATGATGCAGTCTGGCCGGAAAGGGGCGGATATTATGTACACTGGGACGGTGGACTGCTGGAGGAA GATTGCAAAAGATGAGGGAGCCAAGGCTTTCTTCAAAGGTGCCTGGTCCAATGTGTTGAGAGGCATGGG CGGAGCTTTCGTATTGG

SEQ ID. NO.: 103

pKVC59B: Homologous to Rat scg10; Accession SCG1 RAT.

SEQ ID. NO.: 104

pKVC55: Homologous to Human LAMP-1; Accession HSLAMP1A

AGCATGCTGATCCCCATTGCCGTGGGCGGCCTGCGGGGGCTGGTCCTCATCGTCCTCATTGCCTACCTC
ATCGGCAGGAAGAGGAGCCACGCGGCTACCAGACGATCTAGCAGGGCTGCGACACGTCGGGCCGGCTGC
CACTTCCGGTCCTCCGCTCCCCTGAGCTTAGGTTGGCGTGGAGGGCGGCACGTTTCTTGCAAACTG
ATTTTCAAATCTGCTTTATCCGATGTGAAGTTCATCTTGCAACATTTACTATGCACAAGAGTATTGAAA
TGAC

SEQ ID. NO.: 105

pKVC47B: Homologous to Human 71 kD heat shock cognate protein;

Accession HSHSC70

CCTGAGAATAGGTCTAGCATTGTTCCACACAAAACATTTGAAGGACCCAAATTTGTAGCAAATTCCATG GCAGTGAAGTTGAGCTGCTATAGTTAATAAACTGGGCATTCTTGATACTTGAATATGGAATATGTGCAC AAGGGAAGTAAATACAACATTGCACTTTATAAGCACTGTATTGTTAAGTGGGAAATGCAATGTCTTTAA AATAAAACTGTATTTAAAATTGGCGCCCCAAAA AAAAA

SEQ ID. NO.: 107

pKVC46B: Homologous to Human 71 kD heat shock cognate protein;

Accession HSHSC70

CCTGAGAATAGGTCTAGCATTGTTCCACACAAAACATTTGAAGGACCCAAATTTGTAGCAAATTCCATG GCAGTGAAGTTGAGCTGCTATAGTTAATAAACTGGGCATTCTTGATACTTGAATATGGAATATGTGCAC AAGGAAAGTAAATACAACATTGCACTTTATAAGCACTGGTATTGTTAAGTGGGGAATGCAATGTGCTTA AATAAAACTGTATTTAAAATTGGCACCAA

SEQ ID. NO.: 108

pKVC35B: Homologous to Human Vacuolar proton ATPase channel:

Accession HSPCHSUCA

SEQ ID. NO.: 109

pKVC27B: Homologous to Rat Cytoplasmic Succinyl CoA synthetase;

Accession RNGLTA

GCGACACGTTCTGTCATTTATGTTCCTCCTCTTTTGCTGCTGCCATCAATGAAGCTGTTGAGGCG GAAATGCCCTTGGTTGTGCATTACTGAAGGTATCCCACAGCAGGACATGGTGCGGGTCAAGCACAAA CTGCTGCGTCAGGGAAAGACCAGGCTGATCGGGCCTAACTGCCCTGGAGTGATCAATCCTGGAGAATGC AAAATTGGCATCATGCTGGCCATATTCACAAGAAAGGAAGAGTTGGTATTGTGTCCAGATCTGGG

SEQ ID. NO.: 110

pKVC22: Homologous to Human clq beta isoform; Accession HSC1QBR GGAAAGATGGGATTGTATGAAACACTGCATTTCACAGCAAAGACCTCAGTCCAGAACACAACACAGGGG ACCAAGTGGATTCAGGTGTGGTCAAAACTCTGGGGATCACAGTGGGGATACCACCTCCAGGGCTGGTGA CAGATTCAGGACCCTCCTGGCACACCCGGGACCCCAGGGATAAAAGGAGAGAAAAGGGCTGCCAGGGCTG GCTGGAGACCATGGCGAGTTTGGGGAGAAGGGA GACCAGGGATTCTGGAATCAGAAA

SEQ ID. NO.: 111

pKVC22B: Homologous to Human Phospholipase A2; Accession HUMPHPLA2 TTCCAGACGGGAGATTGATTGGAAAAAAAAGTAATGTGTTCCATTTAAAATTTTGGTATATGGCATTTT CTGACTTAGGAAGCCACAATGTTTTTGTTCTTGGCCCCATCATGACATTGGGTAGCATTAAGTTTTGTGC TTCCAAATCACTTTTGTTTTTAAGGATTTCTTGATCTTTAT TCTTTCTATTTGTCAGGTGTACAGGATTACCTT TTTTAGCCTTCTGTCTT

SEQ ID. NO.: 113

pKVC18: Homologous to Human Cytochrome oxidase I: Accession MIHSCG GTTATATTGACTCCTACAAACATAATCGTAAAGTGAATCTTTGCTCAAGTGTTGTCAAGGGTATATCCT GAGAATAGGGGGAATCAATGGACGAAGCCTCCTATGATAGCGAATACTGCTCCTATTGACAAGACATAG TGAAAGTGGGCCACTACGTAATATGTGTCGTGAAGAACAATG TCTAGTGAAGAGTTTGCTAGTACA

SEQ ID. NO.: 114

SEQ ID. NO.: 115

pKVC12B: Homologous to Human 90 kD heat shock protein;

Accession HSHSP90R

ACGCTCGTTTTCCAAAGAGAAGAGCGTTGTTTAGAGTAGCGAAATTCGAAGGCTGCTTAGGCGCATTGT AAAGCTGTTGGGGAAATAACTCCACAAGTTTCGTGAGTGGAAATGTAGTGCTCGAAACACACATTCTGCTT TAAAAGGTTGTAACAAATACAAACAAATTTAAAAAAAAGCTCTGACAAATGTTTTGTGTGGGGAAGCGGG GTTCCAAAATACAGGGCGGCCCC

SEQ ID. NO.: 116

pKVC10B: Homologous to Human Cytoskeletal gamma actin;

Accession HSACTCGR

TTGTCATCTCTCAAGAATTGACAACAGATTTTGGTTTTCTACTGTCATGTGGAACATTAGGCCCCAGCTTCGGCTCCTTGTGCGAGGAAAATAAA

pKVC9: Homologous to Human v-fos transformation effector; Accession

HSFTE1A

GCATCTGATGGCCTTAAGGGTCGTGTTTTGAAGTAAGCCTGGCTGATTTGCAGAATGATGAAGTTGCA
TTTAGGAAATTCAAGCTAATTACTGAAGATGTTCAGGGCAAAAACTGCCTGACTAATCTCCATGGCATG
GATCTTACCCGGGACAAAATGTGCTCCATGGTCAAAAAATGGCAGACCATGATTGAAGCTCACGTTGAT
GTCAAAACTACCGATGGGTATTTGCTTCGTCTCTTTTTGTGTCGGTTTTACTAAAAAAACGCAACAATCAG
A

SEQ ID. NO.: 118

pKVC6B: Homologous to Chicken Amphiphysin; Accession GDAMPHIP CCTTCCAGAACCCTGAGGAGCAGGATGAAGGCTGGCTCATGGGCGTGAAGGAGAGTGACCAGC ACCTAGAGCTGGAGAAATGTCGGGGCGTCTTCCCCGAGAACTTCACCGAGCGGGTTCAGTGAGGGCAGC AGCTGCTGAG

SEQ ID. NO.: 119

pKVC6: Homologous to Human TAPA-1: Accession HSTAPA1
TCTACGACCAGGCTTTGCAGCAGGCCGTGGTAGACGACGACGACGACAATGCCAAGGCCGTGGTGAAGA
CCTTCCATGAGACGCTCAACTGCTGTGGCTCCAGCACGCTCTCCGCGCTGACCACCTCCATTCTCAAGA
ACAACCTGTGTCCTTCAGGCAGCACTGTCATCAGCAACTTCTTCAAGGAGGACTGCCACCAGAAGATCG
ATGACCTCTTCTCGGGAAAGCTGTATCTCATTG GCAT

SEQ ID. NO.: 120

pKVC4B: Homologous to Rat alpha internexin; Accession#RNINTLAA CACCTAAAGAGTTGCCAGGTCTCTGTCACACATCTCCATTCACAACAGATAGGGTGTGATGCTTTTACT AAACTTTCTTATCCTAGGACCTGCTGCAATGGTTCAAGGAACTGGAAAGATGCTTTCTCTTCTTCTTC CCCTCACTCCATCCCTGTCTTTACTCCTCAGACTTCCTGTAAAACATTAGTAAGAATAAAAGT CACACGAATCCAC

SEQ. ID. NO.: 121

>pKVC154

ATTTGGCTCAGTGGCAGAGCGCTTGCCTAGGAAGAGCAAGGCCCTGGGTTCGGTCCCCAGCTCCGpoly (A)

SEQ. ID. NO.: 122

>pKVC159

SEQ. ID. NO.: 123

>pKVC151

GTAATTATTGGCTCAACTTTCCTAATTGTCTGTCTACTACGACAACTAAAATTCCACTTCACATCAAAA CATCATTTCGGATTTGAAGCCGCAGCATGATACTGACACTTCGTAGATGTAGTTTGACTATTCCTATAC GTTTCTATCTATTGATGAGGATCCTpoly(A)

>pKVC158

GATTTGGAGAAGCCTTCGCATCAAAACGAGAAGTACGCTCAATTTCCTACTCCTCAACTAACCTAGAAT GACTGCATGGATGCCCCCCCACCCTACCACACTTCGAAGAACCTTCCTACGTAAAAGTTAAATAAGAAA GGAAGGATTCGAACCCCCTACAACTGGTTTCAAGCCAATTTCATAACCATTATGTCTTTCTCAATpoly (A)

SEQ. ID. NO.: 125

>pKVC160

AAGGATAATGCTGTTTATTAAAAATATACTCAGGAAGTCAGGGTATTGATGCAATTTTACATACGCACT TGGGTAGTCTGAAGTTCCATTATTCCAGCAGTTTATATAAATGTTTCAGATCAAAAGAGAAAAACA CTTTACAGAGACCAGCAGTTGCTTATCAGTTTGGTCATGAGTCTGCTTGTAGTAAAAAATAAAACTCCCT CTTGCATTGCTGAAGAATGTCCTT

SEQ. ID. NO.: 126

>pKVC157

CAGCTCCCTAGTACTTTACTATTATTTCACTAATACTAACAACAAAACTAACACACACAAGCACAATAG ACGCCCAAGAAGTAGAAACAATTTGAACAATCCTCCCAGCTGTCATTCTTATCCTAATTGCCCTTCCCT CCCTACGAATTCTATACATAATAGACGAGATTAATAACCCAGTTCTAACAGTAAAAACTATAGGACACC AATGATACTGAAGCTATGAATATCTGACTATAAGACCTATGACTCCTACATAATCCC

SEQ. ID. NO.: 127

>pKVC156

SEQ. ID. NO.: 128

>pKVC153

SEQ. ID. NO.: 129

>pKVC152

>pKVC161

SEQ. ID. NO.: 131

>pKVC162

GAGCTGTTGCCAGTGTAAAGACAGCAAACATGGACACTCTCGCACTGTGCATCACAAAGCTAACAAATC GAAATCTTGAATGCAGTCTGTCCTAAGTCCAGGCAAGTGACAGCCATGTGTGTCTGCAGTGCTGTGTCA CCACGTCCTGCATTGTTGGAGCTGCTGCAGGGACACTGAGATGAGCAGGTTCTTTGGAAAGAACTGTTG TGCTCCTCAAAGCAGTGTTCAGATTTTAAAGGTTCTTAGCCTCCTCAGTTCCTTATGTGGAACTGTAGG ATCCCCTTCATAAATTTTTAAAGTGCTTATGTGGATCCAATTGGTCTACATTTT

SEQ. ID. NO.: 132

>pKVC36BR

CTTTAGAGAAGGCAGGTCTTACAAACACTACAGAAAAGCCGTTTGGACGTAA AAATCCAAGGAGAAAGGAGTCATTAGGAAATGTAACATAGGACACAGAACG CATGTTGTGTGATGGTCCCTTCTCTTCCGTGTGGTTCCAGAATATGCTCCTGAC CCCAGAGCCGCCACCTGAGCGCGCACCGGGAAGGTCACAGACGACTTCAGGC TTCAGGCGCAACGTC

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